

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/S23,729A  
Source: PCT  
Date Processed by STIC: 4-14-06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER:

10/523,729A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2        Invalid Line Length      The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3        Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4        Non-ASCII      The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
  
- 5        Variable Length      Sequence(s)        contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6        PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7        Skipped Sequences  
    (OLD RULES)      Sequence(s)        missing. If intentional, please insert the following lines for **each** skipped sequence:  
                            (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                            (i)       SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                            (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                            This sequence is intentionally skipped  
  
                            Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8        Skipped Sequences  
    (NEW RULES)      Sequence(s)        missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
                            <210> sequence id number  
                            <400> sequence id number  
                            000
  
- 9        Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                            Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                            In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10        Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
  
- 11        Use of <220>      Sequence(s)        missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                            (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12        PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13        Misuse of n/Xaa      "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



PCT

## RAW SEQUENCE LISTING

DATE: 04/14/2006

PATENT APPLICATION: US/10/523,729A

TIME: 10:25:12

Input Set : F:\Sequence Listing 10523729.txt

Output Set: N:\CRF4\04142006\J523729A.raw

3 <110> APPLICANT: akzo nobel n.v.  
 5 <120> TITLE OF INVENTION: novel bacterial expression system  
 7 <130> FILE REFERENCE: 2002.012  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/523,729A  
 C--> 9 <141> CURRENT FILING DATE: 2005-02-04  
 9 <160> NUMBER OF SEQ ID NOS: 9  
 11 <170> SOFTWARE: PatentIn version 3.1  
 13 <210> SEQ ID NO: 1  
 14 <211> LENGTH: 29  
 15 <212> TYPE: DNA  
 16 <213> ORGANISM: Bacillus subtilis  
 18 <400> SEQUENCE: 1  
 19 ttgtaaaggg acaagagctt tggtataat  
 22 <210> SEQ ID NO: 2  
 23 <211> LENGTH: 94  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Bacillus subtilis  
 27 <400> SEQUENCE: 2  
 28 ttgtaaaggg acaagagctt tggtataata taaaattgtg agtaatagaa ttattgctcc 60  
 30 ttgcccatta tgggccgctt agtccaaaag gagg 94  
 33 <210> SEQ ID NO: 3  
 34 <211> LENGTH: 113  
 35 <212> TYPE: DNA  
 36 <213> ORGANISM: Bacillus subtilis  
 38 <400> SEQUENCE: 3  
 39 gatgcagttg taaagggaca agagctttgg tataatataa aattgtgagt aatagaatta 60  
 41 ttgctccttg cccattatgg gccgcttagt ccaaaaggag gtgcaaacag atg 113  
 44 <210> SEQ ID NO: 4  
 45 <211> LENGTH: 20  
 46 <212> TYPE: DNA  
 47 <213> ORGANISM: Bacillus subtilis  
 49 <220> FEATURE:  
 50 <221> NAME/KEY: misc\_feature  
 51 <222> LOCATION: (8)..(8)  
 52 <223> OTHER INFORMATION: N  
 55 <220> FEATURE:  
 56 <221> NAME/KEY: misc\_feature  
 57 <222> LOCATION: (13)..(14)  
 58 <223> OTHER INFORMATION: N  
 61 <220> FEATURE:  
 62 <221> NAME/KEY: misc\_feature  
 63 <222> LOCATION: (17)..(18)  
 64 <223> OTHER INFORMATION: N

Does Not Comply  
 Corrected Diskette Needed

(pg. 1-2) 29

Invalid Response

Same error

PLS explain "N" locations.

See item #9 on error summary sheet, 4/14/2006

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DATE: 04/14/2006

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TIME: 10:25:12

Input Set : F:\Sequence Listing 10523729.txt

Output Set: N:\CRF4\04142006\J523729A.raw

67 <220> FEATURE:  
 68 <221> NAME/KEY: misc\_feature  
 69 <222> LOCATION: (20)..(20) *Same*  
 70 <223> OTHER INFORMATION: N *error*  
 73 <400> SEQUENCE: 4  
 W--> 74 atttaatatnta tannatnnan 20  
 77 <210> SEQ ID NO: 5  
 78 <211> LENGTH: 33  
 79 <212> TYPE: DNA  
 80 <213> ORGANISM: Bacillus subtilis  
 82 <220> FEATURE:  
 83 <221> NAME/KEY: misc\_feature  
 84 <222> LOCATION: (6)..(6)  
 85 <223> OTHER INFORMATION: N  
 88 <220> FEATURE:  
 89 <221> NAME/KEY: misc\_feature  
 90 <222> LOCATION: (21)..(21)  
 91 <223> OTHER INFORMATION: N  
 94 <220> FEATURE:  
 95 <221> NAME/KEY: misc\_feature  
 96 <222> LOCATION: (26)..(27)  
 97 <223> OTHER INFORMATION: N  
 100 <220> FEATURE:  
 101 <221> NAME/KEY: misc\_feature  
 102 <222> LOCATION: (30)..(31)  
 103 <223> OTHER INFORMATION: N  
 106 <220> FEATURE:  
 107 <221> NAME/KEY: misc\_feature  
 108 <222> LOCATION: (33)..(33)  
 109 <223> OTHER INFORMATION: N  
 112 <220> FEATURE:  
 113 <221> NAME/KEY: misc\_feature  
 114 <222> LOCATION: (11)..(13)  
 115 <223> OTHER INFORMATION: N  
 118 <400> SEQUENCE: 5  
 W--> 119 ttatttnattt nnnatttaatt ntatannatn nan 33  
 122 <210> SEQ ID NO: 6  
 123 <211> LENGTH: 33  
 124 <212> TYPE: DNA  
 125 <213> ORGANISM: Bacillus subtilis  
 127 <400> SEQUENCE: 6  
 128 ttatttcattt ccgatttaatt gtataggatg cag 33  
 131 <210> SEQ ID NO: 7  
 132 <211> LENGTH: 43  
 133 <212> TYPE: DNA  
 134 <213> ORGANISM: Bacillus subtilis  
 136 <400> SEQUENCE: 7  
 137 aaaagtacat atttcttcaa aggaaaaaag caaaagatgt ttt 43  
 140 <210> SEQ ID NO: 8

*See item #9 on error summary sheet*

*Same error*

## RAW SEQUENCE LISTING

DATE: 04/14/2006

PATENT APPLICATION: US/10/523,729A

TIME: 10:25:12

Input Set : F:\Sequence Listing 10523729.txt

Output Set: N:\CRF4\04142006\J523729A.raw

141 &lt;211&gt; LENGTH: 154

142 &lt;212&gt; TYPE: DNA

143 &lt;213&gt; ORGANISM: Bacillus subtilis

145 &lt;400&gt; SEQUENCE: 8

146 aaaagtacat atttcttcaa aggaaaaaag caaaagatgt ttttagctga aggaaaaatg 60

148 aaaacgaaag ataaaaacag aggctgaaag ccatttttaa gcgtttttct tttcttggtg 120

150 catcatttac aatacatata accgcaagga gagg 154

153 &lt;210&gt; SEQ ID NO: 9

154 &lt;211&gt; LENGTH: 166

155 &lt;212&gt; TYPE: DNA

156 &lt;213&gt; ORGANISM: Bacillus subtilis

158 &lt;400&gt; SEQUENCE: 9

159 aaaagtacat atttcttcaa aggaaaaaag caaaagatgt ttttagctga aggaaaaatg 60

161 aaaacgaaag ataaaaacag aggctgaaag ccatttttaa gcgtttttct tttcttggtg 120

163 catcatttac aatacatata accgcaagga gaggaggaat cgcacg 166

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/523,729A

DATE: 04/14/2006  
TIME: 10:25:13

Input Set : F:\Sequence Listing 10523729.txt  
Output Set: N:\CRF4\04142006\J523729A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; N Pos. 8, 13, 14, 17, 18, 20  
Seq#:5; N Pos. 6, 11, 12, 13, 21, 26, 27, 30, 31, 33

VERIFICATION SUMMARY

DATE: 04/14/2006

PATENT APPLICATION: US/10/523,729A

TIME: 10:25:13

Input Set : F:\Sequence Listing 10523729.txt

Output Set: N:\CRF4\04142006\J523729A.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:74 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0

L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0